SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lobb, Roy R.
- (ii) TITLE OF INVENTION: Treatment for Asthma
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 60 State Street, Suite 510
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-1875
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/374,331
 - (B) FILING DATE: 18 JAN 1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/256,631
 - (B) FILING DATE: 12-JUL-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/821,768
 - (B) FILING DATE: 13-JAN 1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US93/00030
 - (B) FILING DATE: 12-JAN-1993
 - (C) APPLICATION NUMBER: US 07/821,768
 - (D) FILING DATE: 13-JAN-1992
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Myers, Louis (PLM)
 - (B) REGISTRATION NUMBER: 35,965
 - (C) REFERENCE/DOCKET NUMBER: D002 CIP PCT (BGP-021US)
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)227-5941
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid

			ANDEDNI OLOGY :		single ear
(ii)	MOLE	CULE	TYPE:	cDNZ	A

(ix) FEATURE:

(A) NAME/KEY: CDS(B) LOCATION: 1..360

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy chain variable region; amino acid 1 is Glu (E) but Gln (Q) may be substituted"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

								GCC Ala 15		48	
						_		ACC Thr		96	
		 						ATT Ile	_	144	
		 	 					TTC Phe		192	
		 -						TGG Trp		240	
								TGT Cys 95	_	288	
								GGC Gly		336	
	ACC Thr									360	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
- Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser 1 5 10 15
- Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
 20 25 30
- Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
 35 40 45
- Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
 50 55 60
- Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu 65 70 . 75 80
- Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95
- Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
 100 105 110
- Gly Thr Thr Val Thr Val Ser Ser 115 120
- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..318
 - (D) OTHER INFORMATION: /note= "HP1/2 light chain variable region"
 - (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light chain variable region"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly

1				5					10					15		
			ACC Thr 20													96
			TAC Tyr													144
			TCC Ser													192
			GGG Gly													240
			GCA Ala													288
			GGG Gly 100													318
			(B)	LEN TYI TOI	GTH: PE: & POLOG	: 106 amino SY:]	ami aci	ino a id ar		5						
	(>	i) S	SEQUE	ENCE	DESC	CRIPT	ION:	: SEÇ) ID	NO:4	l :					
Ser 1	Ile	Val	Met	Thr 5	Gln	Thr	Pro	Lys	Phe 10	Leu	Leu	Val	Ser	Ala 15	Gly	
qaA	Arg	Val	Thr 20	Ile	Thr	Cys	Lys	Ala 25	Ser	Gln	Ser	Val	Thr 30	Asn	Asp	
/al	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Gln	Ser	Pro	Lys 45	Leu	Leu	Ile	
Гуr	Tyr 50	Ala	Ser	Asn	Arg	Tyr 55	Thr	Gly	Val	Pro	Asp 60	Arg	Phe	Thr	Gly	
Ser 65	Gly	Tyr	Gly	Thr	Asp 70	Phe	Thr	Phe	Thr	Ile 75	Ser	Thr	Val	Gln	Ala 80	
3lu	Asp	Leu	Ala	Val 85	Tyr	Phe	Cys	Gln	Gln 90	Asp	Tyr	Ser	Ser	Pro 95	Tyr	
Thr	Phe	Gly	Gly 100	Gly	Thr	Lys	Leu	Glu 105	Ile							

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lobb, Roy R.
- (ii) TITLE OF INVENTION: Treatment for Asthma
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 - (B) FILING DATE: 12-JUL-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/821,768
 - (B) FILING DATE: 13-JAN 1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US93/00030
 - (B) FILING DATE: 12-JAN-1993
 - (C) APPLICATION NUMBER: US 07/821,768
 - (D) FILING DATE: 13-JAN-1992
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Myers, Louis (PLM)
 - (B) REGISTRATION NUMBER: 35,965
 - (C) REFERENCE/DOCKET NUMBER: D002 CIP PCT (BGP-021US)
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617)227-7400
 - (B) TELEFAX: (617)227-5941
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS:	single
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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS(B) LOCATION: 1..360

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy chain variable region; amino acid 1 is Glu (E) but Gln (Q) may be substituted"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAA Lys								48
AAG Lys								96
CAC His								144
 ATT Ile 50	 	 	 _	-				192
AAG Lys								240
CTC Leu								288
GGA Gly								336
 ACC Thr	 							360

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser

1 10 15

Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr

Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly 35 40 45

Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
50 60

Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu 65 70 75 80

Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala 85 90 95

Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser 115 120

- (2) INFORMATION FOR SEQ ID NO:3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..318
 - (D) OTHER INFORMATION: /note= "HP1/2° light chain variable region"
 - (ix) FEATURE:
 - (A) NAME/KEY: misc feature
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light chain variable region"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly

1				5					10					15		
GAC	AGG			ATA	ACC Thr				AGT					AAT		96
,			20		CAG	_	_	25					30		_	144
					Gln											144
					CGC Arg											192 a
AGT	GGA	ТАТ	GGG	ACG	GAT	TTC	ACT	TTC	ACC	ATC	AGC	ACT	GTG	CAG	GCT	240
					Asp 70											
					TAT											288
					Tyr											
					ACC						~	~~			•	/318
Thr	Phe	Gly	Gly 100	Gly	Thr	Lys	Leu	Glu 105	Ile	•	\$\(\)	1	. 7			
								-00			16	المؤثر	1.5	Joan .	_	and and
(2)	INFO)RMA'I	rion	FOR	SEQ	ID N	10:4:	:			5	-	· 0 !	ار ارم درد	1	
	((i) S	(A)	LEN	CHAI GTH :	: 106	ami	ino a		5	ار پر در کور	$C\zeta$	ر .	<u></u>	(_) 	
	((i) S	(A) (B)	LEN TYP	NGTH: PE: a	: 106 amino	ami aci	ino a id		\$? "S	A. A.)) ^	·/		(پر	
			(A) (B) (D)	LEN TYP TOP	NGTH:	: 106 amino 3Y:]	ami aci linea	ino a id ary					ر م ماريخ		() 	
	(i	Li) M	(A) (B) (D)) LEN) TYP) TOP CULE	NGTH: PE: & POLOG	: 106 amino 3Y:] E: pr	ami aci linea cotei	ino a id ary	Cids	2		つく (人)				
Ser	i) c)	ii) M	(A) (B) (D) (D)) LEN) TOP CULE ENCE	NGTH: PE: & POLOG TYPE DESG	: 106 amino GY:] E: pr	ami o aci linea cotei	ino a	in	NO:4	,	Val	Ser	Ala	Gly Gly	
Ser	i) c)	ii) M	(A) (B) (D) (D)) LEN) TOP CULE ENCE	NGTH: PE: & POLOC TYPE	: 106 amino GY:] E: pr	ami o aci linea cotei	ino a	in	NO:	,	you val	Ser	Ala V15	Gly	
1	(i (x Ile	ii) M ki) S Val	(A) (B) (D) MOLEC SEQUE) LEN) TYP) TOP CULE ENCE Thr 5	NGTH: PE: & POLOG TYPE DESG	: 106 aminc GY:] E: pr CRIPT	ami aci linea rotei rION:	ino a id ir in SEG	TID Phe IO	NO:4	Leu	0 (3		- 3 %		
1 Asp	(i (x Ile Arg	ii) M ci) S Val Val	(A) (B) (D) MOLEC SEQUE Met Thr 20) LEN) TYP) TOP CULE ENCE Thr 5	NGTH: PE: a POLOG TYPE DESG	: 106 amino GY: 1 E: pr CRIPT Thr	o aci linea rotei rotei Pro	ino a did ar SEQ Ala .25	icids [ID] [Phe IO] [Ser] [Quantum Phi III Phi II	NO:	Leu	Val.	Thr	Asn	Asp	
1 Asp Val	(i (x Ile Arg Ala	ii) M ci) S Val Val Trp 35	(A) (B) (D) MOLEO SEQUE Met Thr 20	LENCE Thr S Ile	NGTH: PE: & POLOG TYPE DESC Gln Thr	: 106 amino GY:] E: pr CRIPT Thr Cys	o acidines lines rotei FION: Pro Lys Pro 40	ino a id in SEQ Lys Ala .25	ID Phe TO	NO:4	Leu	Val C2 Lys (45	Thr 30 Leu	Asn Leu	Asp	
1 Asp Val Tyr	(i (x Ile Arg Ala Tyr 50	val Val Trp 35	(A) (B) (D) MOLEC SEQUE Met Thr 20 Tyr Ser	LENCE CULE Thr 5 Ile Gln Asn	NGTH: PE: a POLOG TYPE DESC Gln Thr	: 106 amino GY:] E: pr CRIPT Thr Cys Lys Tyr 55	coteines Pro Lys Pro 40	ino a id ir in SEQ Lys Ala .25 Gly Gly	ID Phe 100 Ser Q Gln	NO:4	Leu Ser Prô Asp	Val.	Thr 30 Leu Phe	Asn Leu Thr	Asp	
Asp Val Tyr Ser 65	(ii (x Ile Arg Ala Tyr 50	ii) M ci) S Val Val Trp 35 Ala	(A) (B) (D) MOLEG SEQUE Met Thr 20 Tyr Ser	LENCE THY TOE CULE Thr 5 Ile Gln Asn	NGTH: PE: a POLOG TYPE DESC Gln Thr Gln Arg	: 106 amino GY: 1 E: pr CRIPT Thr Cys Lys Tyr 55 Phe	Fro Lys Pro A0 Thr	ino a id in SEG Lys Ala ,25 Gly Gly	ID Phe TOY Ser Oln Val	NO:4 Leu Ser Pro Ile 75	Leu Ser Prô Asp 60	Val Cys (45) Arg	Thr 30 Leu Phe Val	Asn Leu Thr	Asp Tle(